

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

SUMMARIES

[illegible]

ALIGNMENTS

RESULT	1
LOCUS	AK010252
DEFINITION	AK010252 1450 bp mRNA HTC 05-JU
ACCSSION	Mus musculus ES cells cDNA, RIKEN full-length enriched clone:2400002D05, full insert sequence.
VERSION	AK010252
KEYWORDS	AK010252.1 GI:1284555
SOURCE	CAP trapper. Mus musculus (strain:C57BL/6J) ES cells cDNA to mRNA, clone:11b;RIKEN full-length enriched mouse cDNA library clone:2400002D05.
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euv

REFERENCE	1 (bases 1 to 1450)
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Methods in enzymology. 303, 19-44 (1999)
URL	99279253
PUBMED	10349636
REFERENCE	2 (bases 1 to 1450)
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-triapper-selected cDNAs to
JOURNAL	prepare full-length cDNA libraries for rapid discovery of new genes
	Genome research. 10 (10), 1617-1630 (2000)

AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiyagi, K.,
Fujikawa, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Matabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Qy	1081	tataccaccacaaagtgtcctttagccctcaacttga	1116
Db	1234	TATAGACACCAAGTGTCAATTAGCTCTTACGCTTTGA	1269

RESULT	2		
LOCUS	A0427239/c	572 bp	DNA
DEFINITION	A0427239.1 Homo sapiens genomic clone 2568B9, DNA		
ACCESSION	A0427239		
VERSION	A0427239.1	GT:4499942	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		

BASE COUNT ORIGIN	a	c	g	t
134	157	104	177	

Query Match	35.7%;	Score 398.8;	DB 13;	Length 572;
Best Local Similarity	85.8%;	Pred. NO. 8.9e-94;		
Matches 491; Conservative	0;	Mismatches 72;	Indels 9;	Gaps 4;

Accession	Sequence	Length
QY	lcaagaaccttctgggaacctcgltcaagaagcccaagctctggcagaagaagaagctg	97
Db	TCAAGCGCTTGTGGAAACCTGTGTCAAAAAGCAC -AAGTTGGCAACAAAGAGGCGAC	51.3
QY	aaagccttgaaaagagcgctctgagaagaataaagagagagcttgaaactctgtgcgaat	157
Db	AAATCTTGAACAAGTGCATCAACAAAAGAACAAAGAGAGAGATGGCCCCCTTGAGTCAAGT	45.5

07 158 gcagaggaagagggcatccccagggcttata----ctgcaagaatgcttcataagaca-- 211

Db 452 GCAGAGGAAGGSCATCTCTGGGGCTAGTACTGGCTGGGATAGTGCTTCATACACATT 393

QY	212	-ccagcgctgcgctctctggacaagattgaaagacaactccacaagcagttcaact	270
Db	392	CATGACATCGAGCTTCTGGAAAAATATGAAAAGAAACCTCTCAACAGCAGAGTTCCTT	333
QY	271	cccaagacaaagcacaagcaggaagcgccttctgttgaactcttggggagacatgg	333

Db	332	CCGAGGACGAGGACCAATGAGCAGCTGTTTGTTGGCTTTCCGGGAGTACGG	273
QY	331	acggagctccccaatctcatctgaaagagcagacaacacctgagagaatggtacataagcaat	390
Db	272	ACGGAGCTGCCAATTTGTTTAAAGGAGCGACGACGACCTGAGGAATGGCATGTATGGCAC	213
QY	391	acctgattcaaatcattccatatactatctagttatttccaagcgatagaaatctcgat	450
Db	212	ACCTGATTCAAATTTACTCCACATATATTGAGCGTGTTCAMGCGATGGAATTCAGAT	153
QY	451	ctcgccaataaaccaatctcacctcttcacgcagaatctggttcttgtaagaacctgaa	510
Db	152	CTGCGCAAGAAACAAATCTACATTTTCCAGCTGAACCTGATGTGTTTAAAGAACCTGAA	93
QY	511	gaactcaatitgggttctcaactactctgaagagcaatctcccaagaattggagatgtgaa	570
Db	92	TAACTCAATGTGATTTCAACTATCTGGAAGAGCATTCCTCCAGAGCTGGGAAATGTG - A	34
QY	571	aatctagagagactgattggttcttgaaact	602
Db	33	AATCTAGGAGGACGTGATTTCTTGGAATCT 2	

RESULT	3
LOCUS	AQ427288/c
DEFINITION	AQ427288 560 bp DNA GSS 24-MAR-1999 CITB1-EI-256BD1.Tr CITB1-EI Homo sapiens genomic clone 256BD1, DNAA
ACCESSION	AQ427288
VERSION	AQ427288
KEYWORDS	AQ427288.1 GI:4500038
SOURCE	GSS.
ORGANISM	human. Homo sapiens

Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hunngen/bac_end_search/bac_end_search.html. Seq primer: MJ3 Reverse
Class: BAC ends.

```

source
1. .560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="2568D1"
/clone_lib="CIRBI-E1"
/sex="male"
/cell_type="sperm"
/notes="Vector: pbeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT      132 a      154 c      101 g      173 t
ORIGIN

Query Match      34.5%; Score 384.6; DB 13; Length 560;
Best Local Similarity 85.2%; Pred. No. 4,6e-90;
Matches 478; Conservative 0; Mismatches 74; Indels 9; Gaps 4

0Y      49 ttgggaacctcgttgcagaagccacaagcttggcagaagaagaggttggaaagcttgag 108

```

```

Db      560  TGGGAACCTGTGTCAAGAGCAC-TAGTTGGCAGAAAGAGCGCAAAAGCTCTTGAG 502
Oy      109  aagagcgcccttgagaagaataaaggagagtgaaacttctgagcgaatcgagaggaag 168
Db      501  AAGATGCATCAGAAAAGCAAGAGAGAGTGCCCTTGAGTCAAGTGCAGAGAGAA 442
Oy      169  ggcaccccccaagctgtata---ctgcaagaatggcttcataaaca---ccagcgtgcg 221
Db      441  GGCATCTCTCGTGGCTGAGACTGCTGGATGAGTGGCTTCATAGACATTCATAGCATGCA 382
Oy      222  gctcttgacaagaattgaaagaacactctcaagcgcaagagttcaacttcccaagacag 281
Db      381  GCTTGTGAAAAGATAGAAAAGAGAGCTCTCAAGGCAAGAGTCACTTCCCAAGAGACG 322
Oy      282  aggcacaagcgagcagctgctgttcttgaaacttctgagcgagcactgagcagctccc 341
Db      321  AGGCAAAAGAGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 262
Oy      342  agatcattgaagagacacacacactgagagaatggtacataagaacaacacttgatca 401
Db      261  AGATTGTGTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 202
Oy      402  aatcttccataataatctgatttctcaagcgatgagaatctcgatctgcaaaaaa 461
Db      201  AATTACTCCACATATATATATATATATATATATATATATATATATATATATATATATAT 142
Oy      462  ccaactccacactctcagcagaagaatcggtgtcttgagaacccggaagaacaaatgt 521
Db      141  ACAATTCACATTTTCCAGCTAAACTAGTGTGTGAAGAACCTGAAATTAATCTAATCT 82
Oy      522  ggggttctbaatctcgaagagagctctcctcaggaatgagagatctgaaatctagag 581
Db      81  GATTTCAACTATCTGAAGAGCATCTCCAGAGCTGGAGATGTGTG-AAATCTAGAGGG 23
Oy      582  actgagtgtctggaatct 602
Db      22  ACTGATGTTCTGGAATCT 2

RESULT 4
AA416235 526 bp mRNA EST 16-OCT-1997
LOCUS vF38D07.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:846037
DEFINITION 5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-I GENE PRODUCT ; mRNA sequence.
ACCESSION AA416235
VERSION AA416235
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 526)
Marras, S., Kucaba, T., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The Mashu-NHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-NHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINT ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:498189
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 482.

```

```

FEATURES
    source
        Location/Qualifiers
            1..526
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:846037"
                /sex="male"
                /clone_lib="Soares mouse NBMH"
                /tissue_type="heart"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
                /note="vector: pUT3D-Pac (Pharmacia) with a modified
                polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer [5'
                TGTTACCAATCTGAAAGTGGAGCGCGCGGAGGAGTGTGTGTGTGTGTGTGTGT
                3']; double-stranded cDNA was ligated to Eco RI adaptors
                (pharmacia), digested with Not I and cloned into the Not
                I and Eco RI sites of the modified pUT3D vector. RNA
                provided by Dr. Minoru Ko, Wayne State Univ. Library
                constructed and normalized by Bento Soares and M.Patima
                Bonaldo."
BASE COUNT 140 a 122 c 130 g 134 t
ORIGIN
Query Match 32.9%; Score 367.6; DB 10; Length 526;
Best Local Similarity 81.2%; Pred. No. 1.3e-85;
Matches 427; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Oy 520 gtgggttccaactatcgaagagcattccctcagaatggagagatggaatcctaag 579
Db 1 GTGAGTTTAAACATTTAAAGAGTATTCCTCCCGGAGCTAGAGACTGTGACATCTAGAG 60
Oy 580 agactggaatgtctcgaatactagaataatgaagagcgcgccttgaaatgaatcttg 639
Db 61 AGACTGGAATGTCTGGGAATCTGGACCTGATGATCTCCCTTGAATTAAGTAATTTG 120
Oy 640 aagcaagttacattgtatagatactcagaacaagaagtttccagtgctcccaatctg 699
Db 121 AAGCAAGTTACATTTGTGATATCTCTCGAACAAGTTCTCCAGCGTCTATCTGTCTC 180
Oy 700 ctggagatggaatcttcagtgatgtgtatctcagcaataactcagcagcagctggc 759
Db 181 CTGGGAGTGTGCTGTCTCAGAGGCTGTGATATCAGACAAACAATCTAGTACCTGCA 240
Oy 760 caagatagacagcgtagagagagctgcagagccttctctgtatataaacaagttagc 819
Db 241 CAAGATATAGACAGGCTGGAAGAGCTACAGGTTCTGCTGATTAATAACAAGCTGACC 300
Oy 820 taacttccattcagatgctgaacctgaagaagctcactctgtagtctcagtgaggac 879
Db 301 TACCTTCTCAAGCATCTCAACCTCAAAAAGCTCACCTTGCTGTGTCAGTGGGAT 360
Oy 880 cattggagagctcccaacgcttcttgatgcatcactcagcacttaaatcttgtagc 939
Db 361 CACTGTGGAGAGTCCACCGCCCTTGCGATGCTCTCAAGCCTTTAAATTTTGAAGC 420
Oy 940 ctatgagacaatctcattgataatgccaatgctgaagatggcaatgaataatgaagaat 999
Db 421 CTTGTGACAAATGCCATTGATTAAGACCGGATGTAAGACACTGAAGACAGTAGAGAGC 480
Oy 1000 gaagggatggccaacatttgataagaagattgaagaacctata 1045
Db 481 GAGCGGAGCCCGCAGCATTTGATTAAGAAATTTGAAGCATATTA 526

RESULT 5
AA422330 483 bp mRNA EST 16-OCT-1997
LOCUS vF45D09.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:846713
DEFINITION 5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER
FLIGHTLESS-I GENE PRODUCT ; mRNA sequence.
ACCESSION AA422330

```

VERSION	AA422330.1	GI:2101146
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 483)	
AUTHORS	Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.	
TITLE	The WashU-HHMI Mouse EST project	
JOURNAL	Unpublished (1996)	
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:498865 Seq primer: -28m13 rev2 EF from Amersham High quality sequence stop: 479.	
FEATURES	Location/Qualifiers	
SOURCE	1..483 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:846713" /clone_lib="Soares mouse NBMH" /sex="male" /tissue_type="heart" /dev_stage="4 weeks" /lab_host="DH10B" /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGAGAGGAGCGCGCCGCAAGATTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Patima Bonaldo."	
BASE COUNT	125 a 115 c 120 g 123 t	
ORIGIN		
Query Match	29.0%; Score 323.2; DB 10; Length 483;	
Best Local Similarity	80.6%; Pred. No. 5.2e-74;	
Matches 390; Conservative 0; Mismatches 93; Indels 1; Gaps 1;		
QY	520 gtgggttcaactatcgaagagcattctccagaattggagagattgtaaatctagag	579
Db	1 GTGAGTTTAAACCAATTTAAGAGATATTC -CCGAGCTAGAGACTGTGACACATCTAGAG	59
QY	580 agactggttttctcggaactcgaatctagaagcctgcgcctttgaattagaattg	639
Db	60 AGACTGGACTGTCTCGGAATCTGGACCTGTGATGATCTCCCTTTGAATTAAGTAAATTG	119
QY	640 aagcaagtataattgtgatatactccagcaacaagtttccagtgctccaactctgtc	699
Db	120 AAGCAAGTTAATTTGTGTGATATCTCTCGCAACAAGTTCTCCAGCGTTCCTATCTGTCTC	179
QY	700 ctgcgagatcgaatttcagtggttggatatacagcagagcaataactcagcagacctgcg	759
Db	180 CTGCGAGTGTGTCGCTCGACAGTGCTGGAATACACACCAACAATCTGAGAGACTGCCA	239
QY	760 caagataagacaggtctagagagctcgcagagcttctctgtataaacaagtgcac	819

```

Db      240  CAAATATTAGACAGGCGTGAAGAAGCTAACAAAGTTTCCTGTATTATAAACAAGCTGAC 299
QY      820  tacctccattcattccatgctgaacacctgaagaagctcaactctgttagtgcagtgaggac 879
        |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db      300  TACCTTGCTCAAGGCATGCTCAACCTCCAAAACACTCACCTTGCTGGTTGTCTAGTGGGAT 359
QY      880  catttgtgagctcccctaactgccttttgatacctataccaacccttaaaatttgaac 939
        |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db      360  CACCTGGTGGAGGTCGCCGACCCTCCTCGTAGAGCTCCACGACCTTTGAAATTTGTAAGC 419
QY      940  ctatggacaatccattgatataatgccaatgtaagtcgaatgagcaatgaataatgaagt 999
        |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db      420  CTGTGGACAATCCCATTTGATTAGACCGGATGTCAAGACACACGAAAGACACACTAGAGAC 479
QY      1000 gaac 1003
        ||||
Db      480  GAGC 483

RESULT   6
AQ488137/c    562 bp    DNA    GSS    24-APR-1999
LOCUS       AQ488137
DEFINITION   RPCI-11-264L9, TV RPCI-11 Homo sapiens genomic clone RPCI-11-264L9,
              DNA sequence.
ACCESSION   AQ488137
VERSION     AQ488137.1 GI:4674011
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 562)
            Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter
            ,J.C.
            Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
            Unpublished (1997)
            Other-GSSS: RPCI-11-264L9.TJ
            Contact: Shaying Zhao, William Niernan, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbeetlgr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieterdejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (inforesgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.
            Seq primer: T7
            Class: BAC ends.

FEATURES             location/Qualifiers
     source           1..562
                     /organism="Homo sapiens"
                     /db_xref="GBD:7601264"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-264L9"
                     /clone_1lb="RPCI-11"
                     /sex="Male"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACS.6; Site.1: EcoRI; Site.2: EcoRI;
                     RPCI11 Human Male BAC Library"

BASE COUNT          122 a      152 c      119 g      169 t

ORIGIN
Query Match               26.6%; Score 297.4; DB 13; Length 562;
Best Local Similarity    83.5%; Pred. No. 3e-67;
Matches 375; Conservative 0; Mismatches 66; Indels 8; Gaps 3

1 atggagcataaagtgtgtgtcttcgaacattctgcatcagaagccttlyggnaactcgt 60

```

Db 448 ATGGATACAAAGTGTCATATTTTGACATTTCTGTGTCAAGCCTGTGGAAACTGT 389
 QY 61 gTcaagaagccaagaagcttggcagaagaagagtgynaagagcttgaagaagcgccTg 120
 Db 388 GTCAAGAAGCAC -AAGTTTGGCAGAAAGAGGAGGCAGAAAGTCTTGAGAGAGTCATCA 330
 QY 121 gagaagataaagaagagtggaacttTgTgcgaatgcagyaagaaaggaTcccccag 180
 Db 329 GAAAGACAAAGGAGAGGTGGCCCCCTTGAGTCAAGTGCAGAGAGGAAGCACTCTGTG 270
 QY 181 gctgtata----cgcaagaagtgcttcatagaa---ccaagtgtagcttcttgacaa 233
 Db 269 GCTAGATCTGCGCTGGGGATATGTCCTTCATPAGAAATTCATPAGCATGAGCTTCTGGAAA 210
 QY 234 gatTgaagagacaacttccacaagaagagatTcaacttccacaagaagagagcaaaagag 293
 Db 209 GATGAAAGAAAGAACTCTCACAAAGCAGAGATTCACTTCCAAAGCAGCAGAGCAAAATGAG 150
 QY 294 caatgTcgttTgTgttgaacttTcgttgagagcaacttgagacagagctcccaatTcaatgaa 353
 Db 149 CAGTGTGTTGTGTTTGAGACTTCTTGAGGAGTACTGGACGAGCTGCCAATTTGTTAAA 90
 QY 354 ggaagcagaacacacttgagagaaTgTgtacataagaacaaTacttgattcaatcattccTlac 413
 Db 89 GGAGCAGACGCACCTGAGAGATGGCATGATGCGACACCCCTGATTCAAATTAATCTCCAC 30
 QY 414 atatatcagTattttaaagagatgaanaa 442
 Db 29 ATATATTGAGCTGTTTCAAGGAGTGAANA 1

RESULT	7
A0791237/c	
LOCUS	A0791237
DEFINITION	H5_345_A2_F06_T7A Rpci-11 Human Male BAC Library Homo sapiens
VERSION	genomic.fclone Plate=1071 Col=12 Row=K, DNA sequence.
ACCSSION	A0791237
KEYWORDS	GSS.
SOURCE	A0791237.1 GI:5698784
ORGANISM	GSS. human, Homo sapiens

REFERENCE AUTHORS	TITLE
1 (bases 1 to 453) Mahairas G.G., Wallace J.C., Smith R., Swartzell S., Holzman T., Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and Hood L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589	Contact: Mahairas GG, Wallace JC, Hood L

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPII-11. For BAC library availability, please contact Pieter de Jong (pieter@eojng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics ([info@resgen.com](http://www.hnsc.washington.edu)). BAC end Web Server: <http://www.hnsc.washington.edu>
Plate: 1071 row: K column: 12
Seq primer: T7
Class: BAC ends
High quality sequence stop: 453.

FEATURES	Location/Qualifiers
source	1. .453
	/organism="Homo sapiens"
	/db_xref="taxon:9606"

```

/clone="Plate-1071 Col-12 Row-K"
/clone_lib="RPC1-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"
BASE COUNT      116 a      108 c      78 g      146 t      5 others
ORIGIN

```

Query Match	22.5%;	Score 250.6;	DB 13;	Length 453;
Best Local Similarity	83.6%;	Pred. No. 5.1e-55;		
Matches 305;	Conservative 0;	Mismatches 58;	Indels 2;	Gaps 2;
QY 229 gacaagattgaaagaaacactctcaaaagcagattcacttcccaagacagagcaca				
Db 402 GAAAGATGAGAAAGAAAGCTCTCACAAGCGCAGAGATTCACTCCCAAGACAGAGCAAA				
QY 289 cggagcaatggtttgtgtttgaaacttctggggagcactgaggaagctcccaattca				
Db 342 TGGACCAATGTGTTGTGTGTGAATCTTCTGGGGGATGACTGAACGGAGCTGCACAAATTG				
QY 349 ttgaagagcagacacacactgagagaatgtaacataagacaataccattgataatcatt				
Db 282 TTATNAGAGCAGACGCCACTTGAGAGAAATGGCATGTATGCGACACCATATTCAATTACT				
QY 409 cctacatatattcagtatttccaagcgataggaaattctgtagatctgycacaaaaaaccaatc				
Db 222 CCCACATTAATGTGAGCTTTTCCAAGCGATGAGAAATTCAGGATCTTCCCAAGAAACAAATTC				
QY 469 tcaactctccaagcagaatcggtgtgtttgaagaaccgaaagaactcaatgtggttc				
Db 162 TCACATTTTCCAGCTAAACCTCAAGTTGTTGAAGAACTTAATAATCAATGTAGAGTTTC				
QY 529 aactactgaagagcattctccagaatttggagatgtgaaatcctagagagactgat				
Db 102 TACTATGTGAAGA-AAAAAAACAGAGCTGGCAGATGTGTG-NNATCTFAGAGNAGTGGNT				
QY 589 tgttc 593				
Db 44 TGTCC 40				

RESULT	8
BEL10536/c	
LOCUS	BEL10536
DEFINITION	BE110536 - 557 bp mRNA EST 13-JUN-2000
ACCESSION	U1-R-BJ1-avt-b-09-0-U1 s1 U1-R-BJ1 Rattus norvegicus cDNA clone
VERSION	U1-R-BJ1-avt-b-09-0-U1 3', mRNA sequence.
KEYWORDS	BE110536
SOURCE	BE110536.1 GI:8502641
ORGANISM	EST.
	Norway rat.
	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 557)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene
JOURNAL	discovery
MEDLINE	Genome Res. 6 (9), 791-806 (1996)
COMMENT	97044477
	Contact: Soares, MB

Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mscares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized heart library cDNA library Preparation: M.B. Soares Lab Genome distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=yes.

FEATURES

Location/Qualifiers

1..557
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ1-avt-b-09-0-UI"
/clone.lib="UI-R-BJ1"
/lab.host="DH10B (Life Technologies)"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1 library is a subtracted library derived from the following tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV canal at 15 dpc, ventricle at 13 dpc, and adult heart. For a detailed description of the library, from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-BJ1
TAG_TISSUE=heart
TAG_SEQ=ACAC"

BASE COUNT 136 a 104 c 139 g 177 t 1 others
ORIGIN

Query Match 22.1%; Score 246.6; DB 10; Length 557;
Best Local Similarity 81.8%; Pred. No. 6e-54;
Matches 296; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 755 tcccgcaagatataagcaagctagagagctgagagcttctctgtataaaagaat 814
DB 557 tcccgcaagatataagcaagctgagagctgagagcttctctgtataaaagaat 499
QY 815 tgaactaccctccatcatgctgaagctgaagagctgaagctgctgaagctgctgaag 874
DB 498 tgaactaccctccatcatgctgaagctgaagagctgaagagctgctgaagctgctgaag 439
QY 875 gggaccattggtgagagctcccaactgcccctgtgactcatccacaccttaaaattg 934
DB 438 gggaccattggtgagagctcccaactgcccctgtgactcatccacaccttaaaattg 379
QY 935 taagcctatgacaatcctattgataatgcccacatgtaagctgaagctgaagctgaag 994
DB 378 taagcctatgacaatcctattgataatgcccacatgtaagctgaagctgaagctgaag 319
QY 995 aaagtgaagcggagatcgcaacatttgaataaagaagttaagaagcctatgaagacc 1054
DB 318 aaagtgaagcggagatcgcaacatttgaataaagaagttaagaagcctatgaagacc 259
QY 1055 ttaagaagaagaatcgttccagcctatacacaagaagtgctcttgaagcctcaactt 1114
DB 258 ttaagaagaagaatcgttccagcctatacacaagaagtgctcttgaagcctcaactt 199
QY 1115 ga 1116
DB 198 GA 197

RESULT 9
LOCUS A0729142 462 bp DNA GSS 15-JUL-1999
DEFINITION HS_5467_B2_B10_S6E RPCI-11 Human Male BAC library Homo sapiens
ACCESSION A0729142 genomic clone Plate=1043 Col=20 Row=D, DNA sequence.

VERSION A0729142.1 GI:5500694
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 462)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.bufileo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.bufileo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 1043 Row: D Column: 20
Seq primer: Sp6
Class: BAC ends
High quality sequence stop: 462.

FEATURES

Location/Qualifiers

1..462
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1043 Col=20 Row=D"
/clone.lib="RPCI-11 Human Male BAC library"
/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

BASE COUNT 108 a 127 c 92 g 135 t
ORIGIN

Query Match 21.3%; Score 237.4; DB 13; Length 462;
Best Local Similarity 84.0%; Pred. No. 1.4e-51;
Matches 293; Conservative 0; Mismatches 51; Indels 5; Gaps 2;

QY 605 aattaatgagagctgcccttgaaattgaattgaagaagcttaacttgtagatatc 664
DB 5 aattaatgagagctgcccttgaaattgaattgaagaagcttaacttgtagatatc 64
QY 665 cagcaacaagaatttcacagtgctcccaactcgtgtcctgcgagatgtaattgcaatg 724
DB 65 cagcaacaagaatttcacagtgctcccaactcgtgtcctgcgagatgtaattgcaatg 123
QY 725 tggatatacagcaagaataactgacagcctgcggaagatatagacaagctagagagc 784
DB 124 tggatatacagcaagaataactgacagcctgcggaagatatagacaagctagagagc 179
QY 785 tgcagagcttctcctgtataaaacaagtgactaactcctcattccatgcgaacc 844
DB 180 tgcagagcttctcctgtataaaacaagtgactaactcctcattccatgcgaacc 239
QY 845 tgaagaagctcaactcgtgtagtgcagtgaggagcaattggtgagctcccaactgacc 904
DB 240 tgaagaagctcaactcgtgtagtgcagtgaggagcaattggtgagctcccaactgacc 259
QY 905 ttgtgactcatccacaccttaaaatttgaagcctatgagaatcc 953
|||||

Db 300 TTGTGACTACGACCTTAAATTTGTAAGCTTATAACATCC 348

RESULT 10
 AM488294/c 432 bp mRNA EST 24-FEB-2000
 LOCUS
 DEFINITION UT-M-BH3-ary-h-06-0-UT.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
 UT-M-BH3-ary-h-06-0-UT 3', mRNA sequence.
 AM488294
 VERSION AM488294.1 GI:7058564
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 432)
 REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704447
 COMMENT Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestr@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present to identify it as a clone from the normalized hippocampus library cDNA library preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence: 1-32, >AT-richlow.complexity
 Seq primer: M13 forward
 POLY-A-yes.

FEATURES

Location/Qualifiers

1..432
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UT-M-BH3-ary-h-06-0-UT"
 /clone_id="NIH_BMAP_M_S4"
 /dev_stage="27-32 days"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT7AD-Pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography.

converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG-LIB=NIH_BMAP_M_S4
 TAG-TISSUE=hippocampus
 TAG-SEQ=TCGA*

BASE COUNT 118 a 85 c 83 g 145 t 1 others
 ORIGIN

Query Match 15.1%; Score 168; DB 10; Length 432;
 Best Local Similarly 82.4%; Pred. No. 2.1e-33;
 Matches 192; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db 431 TGTGTGAGGTCCTCCGACCGCCCTTGTGCGTCACGCCCTTTGAAATTTTAAGCCTTG 372
 QY 944 tggacaatcctatgataatgccaatgtgaagatggaatgaaataatggaagtgaac 1003
 Db 371 TGGACAATCCATGTGATAGACCGGATGTCAAGACACTGAAGACACAGTAGAGCGAGC 312
 QY 1004 gggatcgccaacatttgataaagaagtatgaagactatattgaagacctaaagaa 1063
 Db 311 GGGACCGCCACGATTTGATAGGAATTTATGAAGCATATATGAAACCTTAAGAA 252
 QY 1064 gagatcgtgtccagcagctacacccaagaagtgcttttagccttaacctga 1116
 Db 251 GAGAGCTGTTCCTCCAGTTATACGACCAAGTGTATTTAGTCTTACGCTTTGA 199

RESULT 11
 AA500912 443 bp mRNA EST 01-JUL-1997
 AA500912
 LOCUS vq03004.r1 Soares mouse NBMH Mus musculus cDNA clone IMAGE:860263
 DEFINITION 5', mRNA sequence.
 AA500912
 ACCESSION AA500912.1 GI:2235879
 VERSION
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 443)

REFERENCE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Weisling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:504351

Putative full length read
 vector to vector length is
 Seq primer: -28ml3 rev2 ET from Amerisham
 High quality sequence stop: 362.
 Location/Qualifiers

1..443
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:860263"

FEATURES

source


```

/clone_lib="Soares mouse NDKH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
(note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15',
TGTTACCACTCTGAAAGTGGAGCGCCGCCGAAATTTTTTTTTTTTTTTTTT
3') double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pRT3D vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

```

	Query Match	15.0%	Score 167	DB 10	Length 443
	Best Local Similarity	80.8%	Pred. No. 3,8e-33		
	Matches 219	Conservative 0	Mismatches 50	Indels 2	Gaps 2
OY	848	agaagctcactctgtttagtcgltcagltgggagccatttggltga-gctcccaactgcctt	906		
Db	1	AAAACCTTCAACCTCGTGGTTGTCACTGGGGATACACTGTGTGACGCGTCCCGACCCCCCTCC	60		
OY	907	tgtgcatctccacacaccttaaatctttagaccttaatgagacatccatctgataatgcc	966		
Db	61	TGCGATGCGCTCACCACCTTTTGAAATTTGTAACTTGTGGACCAATCCATTATATAAGACC	120		
OY	967	caatgtgaagatgycaatgaaataatggaagaatgaaacggatgcgcaac-atttgataa	1025		
Db	121	GGATGTCAAGACACACGAAGACACACTAGAGACGACGGGACCGCAGCGAGATTGTGATPA	180		
OY	1026	agaagtttgaagaagcctatattgaagaccttaagaagaagaagatctgtttccagctatcc	1085		
Db	181	GGAATTTATGAAGAAGCATATATTGAAGACCTTAAAGAAGAAGAGAGCTGTTCACAGTTATAC	240		
OY	1086	cacccaaatgtctttagaccttcaactttga	1116		
Db	241	GACCAAAAGTGTATTATTAGTCTTCACCTTTTGA	271		

RESULT	12			
LOCUS	BG203142			
DEFINITION	BG203142	377 bp	mrna	EST
ACCESSION	BG203142			21-APR-2001
VERSION	BG203142.1			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1 (bases 1 to 377)			
	Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J., Lemer,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E., Veloso,N., Hess,J., Cotren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducat,M.			
TITLE	Creation of genome-wide Protein Expression Libraries using Random			
JOURNAL	Activation of Gene Expression			
COMMENT	Net. Biotechnol. 19 (5), 440 (2001) In press			
	Contact: Scott J. Cain			
	Athersys, Inc.			
	3201 Carnegie Ave, Cleveland, OH 44115, USA			
	Tel: 216 431 9900			
	Fax: 216 361 9596			
	Email: scain@atersys.com			
FEATURES	High quality sequence stop: 377.			
source	1. location/Qualifiers			

	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_lib="Athersys RAGE library"
	/cell_line="HT1080"
	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT	139 a	66 c	65 g	104 t	3 others
ORIGIN					

Query Match	13.3%	Score 148.2;	DB 11;	Length 377;
Best Local Similarity	96.6%;	Pred. No. 3e-28;		
Matches 172; Conservative	0;	Mismatches	4;	Indels 2; Gaps 2;
OY 939	ccttttgacataccttatgatatgaccacaatgtgaagtcgcagtgaataaatgaaag	998		
Dd 16	CTTCGGNACAATCCTATTGATAAAAGGCC - ATGTAAAGA - GGCAATGAATATATGAAAAG	73		
OY 999	tgaacggcatcgccacaacttattgataagaagttaagaagcctatatgaaggaccttaa	1058		
Dd 74	TGAACGGATCGCCACACTTTTGGATAAAGAAATTTTGAAAAAGCTTATTGANAAGACCTTRA	133		
OY 1059	aaaagagaaatctgtcccagctatacaaccaaacgaatgtctttaagcctccaacttga	1116		
Dd 134	AGAAAGAAATCTGTCTCCACGCTATACCACCAAAGTGTCITTTTAAGCTTCAACTTTGA	191		

RESULT	13
LOCUS	BGI97958
DEFINITION	BGI97958 370 bp mRNA EST 21-APR-2001
ACCESSION	RS117210
VERSION	Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
KEYWORDS	BGI97958
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	1 (bases 1 to 370)
	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Wittington,J., Lener,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E., Veloso,N., Hess,J., Cochren,K., Lo,K., Offenbacher,J., Danzig,U. and Ducat,M.
TITLE	Creation of genome-wide Protein Expression Libraries using Random Activation of Gene Expression
JOURNAL	Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT	Contact: Scott J. Cain
	Athersys, Inc.
	3201 Carnegie Ave, Cleveland, OH 44115, USA
	Tel: 216 431 9900
	Fax: 216 361 9536
	Email: scaine@atersys.com
	High quality sequence stop: 324.
FEATURES	Location/Qualifiers
Source	1..370
	/organism="Homo sapiens"
	/db_xref="caxon:9606"
	/clone_lib="Athersys RAGE Library"
	/cell_line="HT1080"
	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT	137 a 65 c 63 g 104 t 1 others
ORIGIN	

Tue, Feb 26 15:53:36 2002

us-09-602-833a-1_1.rst

Page 11

Search completed: February 26, 2002, 09:57:31
Job time: 16313 sec
